

86758

From: Gibbs, Terra  
Sent: Wednesday, November 20, 2002 7:46 PM  
To: STIC-Biotech/ChemLib  
Subject: Seq search

Could you please do a regular sequence search of SEQ ID NO:1 of Serial no. 09/844915?

**Terra Gibbs #79523**  
**AU 1635**  
**Mailbox 11E12**  
**306-3221**

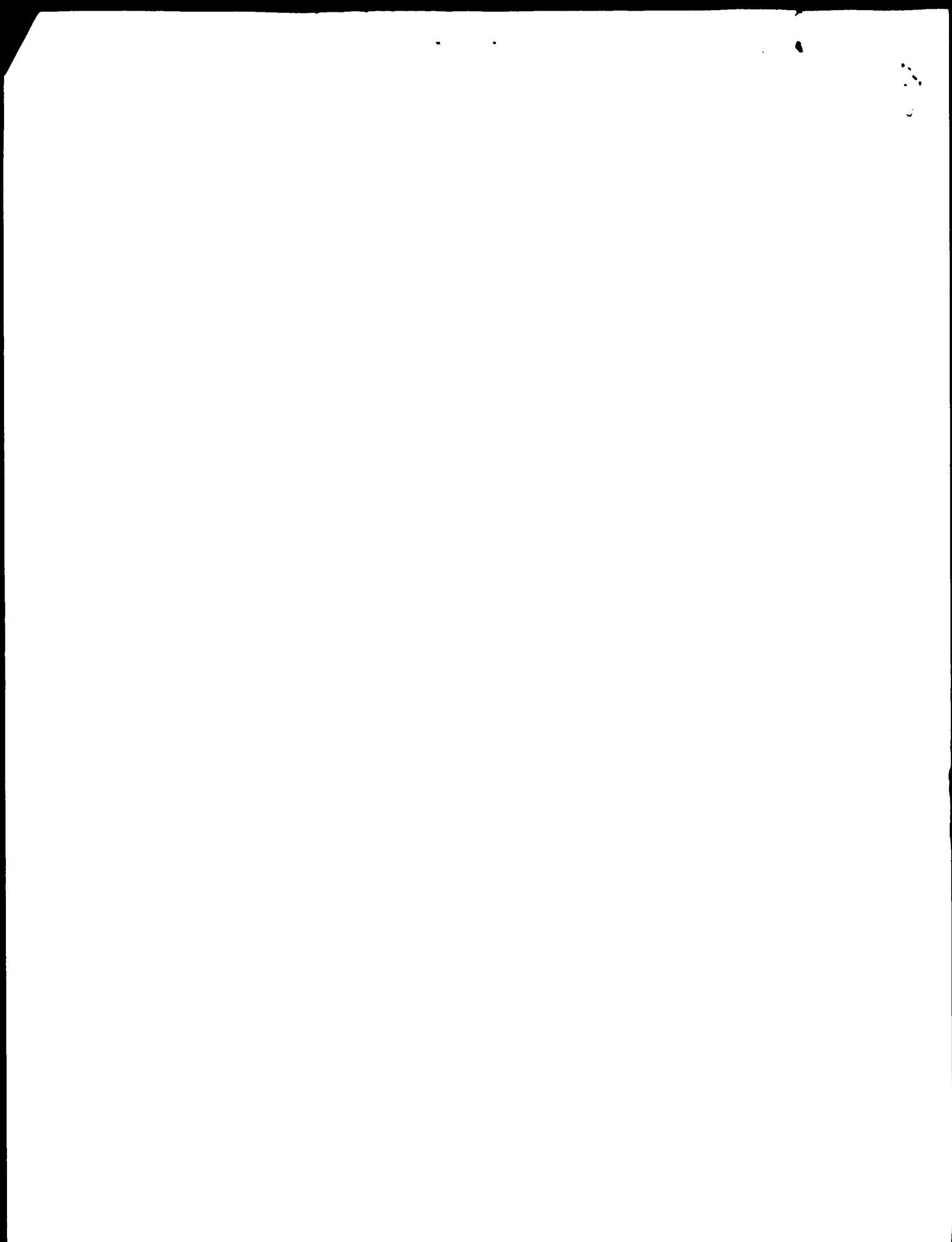
THANK YOU!

Point of Contact  
P. Sheppard  
Telephone number (703) 308-4499

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: 12/3/02  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_





**DEFINITION:** BB558103.03 RIKEN full-length enriched, 2 days pregnant adult female ovary Mus musculus cDNA clone BB558103E13.3, mRNA sequence.  
**ACCESSION:** BB558103  
**VERSION:** BB558103.2  
**KEYWORDS:** EST.  
**ORGANISM:** house mouse.  
**REFERENCE:** Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**AUTHORS:** 1 (bases 1 to 651)  
 Arakawa,T., Carrinci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,N., Kamehara,T., Kanda,M., Koyas,M., Matsuyama,T., Miyazaki,A., Nishimura,Y., Ohno,M., Okazaki,Y., Okido,T., Saito,F., Sakai,T., Sakai,Y., Saito,H., Sasaki,A., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,F., Toyota,T., Muramatsu,M. and Hayashizaki,Y.  
**TIME:** RIKEN Mouse ESTs (Arakawa,T. et al. 2001)  
**COMMENT:** The Enriched (2001)  
 1. And 2. are of this sequence version replaced (J. 944469  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center(GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 240-0045, Japan  
 Tel. 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gs.riken.go.jp,  
 gsc\_http://genome.gsc.riken.go.jp/  
 Catalini,F., Shibata,Y., Hayashi,K., Sugihara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10):1617-1626 (2000)  
 Nagai,Y., Fujiwara,S., Inoue,K., Takaya,Y., Iwama,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Orawa,K., Tanaka,T., Matsura,S., Kawai,N., Okazaki,Y., Muramatsu,M., Inoue,Y., Kito,A. and Hayashizaki,Y.  
 RIKEN integrated sequence analysis (RISA) system--384 format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11): 1757-1771 (2000)  
 Kondo,H., Fukushiro,Y., Shibata,K., Itoh,M., Carrinci,P., Sugahara,Y. and Hayashizaki,Y.  
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (12): 2019-2031 (2001)  
 Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yananaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,N., Shibata,K. and Hayashizaki,Y.  
 Configurational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome.* 12, 673-677 (2001)  
 Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.  
 cDNA library was prepared and sequenced in Mouse Gen. me Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Facility in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
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 /sex="female"  
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 /lab\_host="DH10B"  
 /note="Site 1: Saito; Site 2: BanH; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Facility in Riken"



clone UNCGWV101E15-3', cDNA sequence.

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VERSION  
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KEYWORDS  
EST  
SOURCE  
house mouse  
ORGANISM  
Mus musculus

REFERENCE  
1 (bases 1 to 311)  
Fukuyama, T., Kishida, S., Akahira, S., Akaiyama, J., Akakawa, T., Carrinchi, P., Endo, H., Fukuda, S., Fukushiki, Y., Hara, A., Hayatsu, H., Higashino, T., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Iwata, Y., Kadoya, Y., Kadowa, I., Kato, C., Kawabuchi, Y., Kikuchi, M., Miyasaka, H., Nishida, T., Nishida, S., Kaya, S., Kikuchi, C., Kusakabe, M., Matsuyama, T., Miki, P., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ohtsuki, T., Owa, T., Saito, H., Sakai, C., Saito, Y., Shibata, K., Shibata, Y., Shigematsu, Y., Shinagawa, A., Shitaki, T., Sugabe, Y., Sugihara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tanihara, N., Toya, T., Tsunoda, Y., Watanabe, A., Watanabe, S., Yamamura, T., Yamakawa, I., Yano, F., Yoshida, A., Yokota, I., Yoshida, K., Yoshida, A., Yoshida, M., Muramatsu, M., and Hayashizaki, Y.  
RIKEN Mouse ESTs (Konno, H., et al.)  
Unpublished (2000)

TITLE  
JOURNAL  
COMMENT

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Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
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Email: genome-res@gscl.riken.go.jp  
URL: http://genome.gsc.riken.go.jp/  
Carrinchi, P., Nishiyama, Y., Watanabe, A., Itoh, M., Nagata, S., Otsuki, M., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
Thermostabilization and thermostabilization of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 96: 500-504 (1999)  
Itoh, M., Kikuchi, T., Akaiyama, J., Shibata, K., Izawa, M., Kawai, J., Tanihara, N., Carrinchi, P., Shibata, Y., Kawai, Y., Muramatsu, M., Okazaki, Y., and Hayashizaki, Y.  
Automated filtration-based high throughput plasmid preparation system. Genome Res. 9: 457-473 (1999)  
Carrinchi, P., and Hayashizaki, Y.  
High efficiency full-length cDNA cloning. Methods Enzymol. 333, 19-44 (1999)  
Please visit our web site (http://genome.riken.go.jp) for further details.

FEATURES  
Location/Qualifiers  
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/note="Site 1: SalI, Site 2: BamHI. cDNA library was prepared and stored in pCM108 in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was cloned with a primer [5', GAGAGAGAGAGATCCAGAGAGCTTTTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence GAGAGAGAGATCCAGAGAGCTTTTCTTTTCTTTTCTTTT 3'. cDNA was cleaved with XhoI and BamHI. Vector: a modified Bluescript KS(+) after bulk excision from Lambda PUC 1." (1) a 5' 3' 5' 3'

clone UNCGWV101E15-3', cDNA sequence.

ACCESSION  
E0236341  
VERSION  
1  
KEYWORDS  
EST  
SOURCE  
house mouse  
ORGANISM  
Mus musculus

REFERENCE  
1 (bases 1 to 113)  
Fukuyama, T., Kishida, S., Akahira, S., Akaiyama, J., Akakawa, T., Carrinchi, P., Endo, H., Fukuda, S., Fukushiki, Y., Hara, A., Hayatsu, H., Higashino, T., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Iwata, Y., Kadoya, Y., Kadowa, I., Kato, C., Kawabuchi, Y., Kikuchi, M., Miyasaka, H., Nishida, T., Nishida, S., Kaya, S., Kikuchi, C., Kusakabe, M., Matsuyama, T., Miki, P., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ohtsuki, T., Owa, T., Saito, H., Sakai, C., Saito, Y., Shibata, K., Shibata, Y., Shigematsu, Y., Shinagawa, A., Shitaki, T., Sugabe, Y., Sugihara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tanihara, N., Toya, T., Tsunoda, Y., Watanabe, A., Watanabe, S., Yamamura, T., Yamakawa, I., Yano, F., Yoshida, A., Yokota, I., Yoshida, K., Yoshida, A., Yoshida, M., Muramatsu, M., and Hayashizaki, Y.  
RIKEN Mouse ESTs (Konno, H., et al.)  
Unpublished (2000)

TITLE  
JOURNAL  
COMMENT

Contract, Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
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Carrinchi, P., Nishiyama, Y., Watanabe, A., Itoh, M., Nagata, S., Otsuki, M., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
Thermostabilization and thermostabilization of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 96: 500-504 (1999)  
Itoh, M., Kikuchi, T., Akaiyama, J., Shibata, K., Izawa, M., Kawai, J., Tanihara, N., Carrinchi, P., Shibata, Y., Kawai, Y., Muramatsu, M., Okazaki, Y., and Hayashizaki, Y.  
Automated filtration-based high throughput plasmid preparation system. Genome Res. 9: 457-473 (1999)  
Carrinchi, P., and Hayashizaki, Y.  
High efficiency full-length cDNA cloning. Methods Enzymol. 333, 19-44 (1999)  
Please visit our web site (http://genome.riken.go.jp) for further details.

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/dev\_stage="2 cells"  
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Best Local Similarity 84.0%, P-val 1e-30,
Matches 217, Conservative 0, Mismatches 4, Indels 0, Gaps 0,
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ACCESSION  AZ361725
VERSION    AZ361725.1  GI:10475425
KEYWORDS   CCC.
SOURCE     house mouse.
ORGANISM   Mus musculus
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  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 643)
REFERENCE   1 (bases 1 to 643)
AUTHORS   Smith, B., Ayala, A., Parker, M., Roach, J., David, B., Hemil, C.,
  Islam, H., Longacre, S., Mahmood, M., Menzies, E., Pedersen, T., Pelly
  M., Rice, M., Rice, E., Stokes, R., Tager, A., van Riederhausen, A.
  and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Silvio R. Weir
  University of Utah Genome Center
  Rm 309, Biomedical Research Bldg., 20 S. 2000 E., Salt Lake
  84142, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0106 Row: J Column: 01
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    Technologies. Note: this is a T1-CAP library."
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Best Local Similarity 84.0%, P-val 1e-30,
Matches 217, Conservative 0, Mismatches 4, Indels 0, Gaps 0,
CY 1 AGGCAATTTTCCTTGGTATTTTC 25
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DL 340 AGGCAATTTTCCTTGGTATTTTC 316

RESULT 13

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10 kb range using preparative agarose gel
electrophoresis. Vector DNA was ligated from a derivative
of pMD42 (g1473011436/AP100021), a copy-number
inducible derivative of plasmid p1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      59 a  97 c  101 g  150 t      1 others
ORIGIN
Query Match      74.4%, Score 18.6, E-17, Length 440,
Best Local Similarity 84.0%, P-val 1e-30,
Matches 217, Conservative 0, Mismatches 4, Indels 0, Gaps 0,
CY 1 AGGCAATTTTCCTTGGTATTTTC 25
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ACCESSION  BG970339
VERSION    BG970339.1  GI:14387976
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SOURCE     house mouse.
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  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 961)
REFERENCE   1 (bases 1 to 961)
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contract: Robert Strausberg, Ph.D.
  Fraile, S. J. (email: nih.gov)
  Tissue Procurement: Jeffrey E. Green, M.D.
  CGA Library Preparation: Life Technologies, Inc.
  CGA Library Arrayed by: The I.M.A.G.E. Consortium (LIDL)
  DNA Sequencing by: Incyte Genomics, Inc.
  Clone Distribution: MGC clone distribution information can be
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    Average insert size: 1.75 kb. Constructed by Life
    Technologies. Note: this is a T1-CAP library."
BASE COUNT      59 a  97 c  101 g  150 t      1 others
ORIGIN
Query Match      74.4%, Score 18.5, E-13, Length 561,
Best Local Similarity 84.0%, P-val 1e-30,
Matches 217, Conservative 0, Mismatches 4, Indels 0, Gaps 0,
CY 1 AGGCAATTTTCCTTGGTATTTTC 25
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DL 340 AGGCAATTTTCCTTGGTATTTTC 316

RESULT 13

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 Job time : 2694 secs



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1 APPLICANT: Giannoukakis, Nick
2 TITLE OF INVENTION: THE USE OF TELESCOPING GENETIC CELLS
3 TITLE OF INVENTION: FOR ENHANCING EFFICIENCY IN A HOST AND METHOD FOR
4 TITLE OF INVENTION: MAPING THE SAME
5 FILE REFERENCE: AB32737 / 0909060225
6 CURRENT APPLICATION NUMBER: US09/844,915
7 CURRENT FILING DATE: 2001-04-09
8 PRIOR APPLICATION NUMBER: 09/844,473
9 PRIOR FILING DATE: 2000-04-22
10 SOFTWARE: FastSeq for Windows Version 4.0
11 SEQ ID NO. 2
12 LENGTH: 25
13 TYPE: DNA
14 ORGANISM: Artificial Sequence
15 FEATURE:
16 OTHER INFORMATION: Cytb (b) (6) (b) (7) (d) (e) (f) (g) (h)
US 09-844-915-2

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2 25 AGGACTTTCCGCTGGGACTTCC 1

RESULT 3
US 09-766-095-44
Sequence 44, Application US/09766095
Patent No. US20010002016A1
GENERAL INFORMATION:
APPLICANT: Sherid H. McDermid, Thomas P. Ryder,
Yeasing Yang
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
METHODS AND PROBES
TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PS/2 Model 502 32 SEBX
OPERATING SYSTEM: IBM PC DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 09/766,095
FILING DATE: 18-Jan-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/013,406
FILING DATE: 28-Jan-01
APPLICATION NUMBER: 09/013,406
FILING DATE: 10-Jul-90
APPLICATION NUMBER: 09/013,406
FILING DATE: 11-Jul-89
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 196/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 673510
INFORMATION FOR SEQ ID NO. 124:
SEQUENCE CHARACTERISTICS:
LENGTH: 27
TYPE: nucleic acid
STRANDEDNESS: single
TOPLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO. 124:
US-09-766-095-124

Query Match 100.0%, Score 25, DB 10, Length 27,
Best local similarity 100.0%, Freq. No. 0.0053,
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 1 AGGACTTTCCGCTGGGACTTCC 25
2 3 AGGACTTTCCGCTGGGACTTCC 27

```

```

1 APPLICANT: Giannoukakis, Nick
2 TITLE OF INVENTION: THE USE OF TELESCOPING GENETIC CELLS
3 TITLE OF INVENTION: FOR ENHANCING EFFICIENCY IN A HOST AND METHOD FOR
4 TITLE OF INVENTION: MAPING THE SAME
5 FILE REFERENCE: AB32737 / 0909060225
6 CURRENT APPLICATION NUMBER: US09/844,915
7 CURRENT FILING DATE: 2001-04-09
8 PRIOR APPLICATION NUMBER: 09/844,473
9 PRIOR FILING DATE: 2000-04-22
10 SOFTWARE: FastSeq for Windows Version 4.0
11 SEQ ID NO. 2
12 LENGTH: 25
13 TYPE: DNA
14 ORGANISM: Artificial Sequence
15 FEATURE:
16 OTHER INFORMATION: Cytb (b) (6) (b) (7) (d) (e) (f) (g) (h)
US 09-844-915-2

Query Match 100.0%, Score 25, DB 10, Length 27,
Best local similarity 100.0%, Freq. No. 0.0053,
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 1 AGGACTTTCCGCTGGGACTTCC 25
2 3 AGGACTTTCCGCTGGGACTTCC 27

RESULT 4
US-09-766-095-124
Sequence 124, Application US/09766095
Patent No. US20010002016A1
GENERAL INFORMATION:
APPLICANT: Sherid H. McDermid, Thomas P. Ryder,
Yeasing Yang
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
METHODS AND PROBES
TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PS/2 Model 502 32 SEBX
OPERATING SYSTEM: IBM PC DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 09/766,095
FILING DATE: 18-Jan-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/013,406
FILING DATE: 28-Jan-01
APPLICATION NUMBER: 09/013,406
FILING DATE: 10-Jul-90
APPLICATION NUMBER: 09/013,406
FILING DATE: 11-Jul-89
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 196/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 673510
INFORMATION FOR SEQ ID NO. 124:
SEQUENCE CHARACTERISTICS:
LENGTH: 27
TYPE: nucleic acid
STRANDEDNESS: single
TOPLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO. 124:
US-09-766-095-124

Query Match 100.0%, Score 25, DB 10, Length 27,
Best local similarity 100.0%, Freq. No. 0.0053,
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 1 AGGACTTTCCGCTGGGACTTCC 25
2 3 AGGACTTTCCGCTGGGACTTCC 27

```

RESULT 5  
US-09-992-964-12

Sequence ID: Affiliation: 0000000000  
Patent No: 00000000000000000000  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin  
APPLICANT: Gurney, Austin  
APPLICANT: Wood, William  
TITLE OF INVENTION: Apo-2DSR  
FILE REFERENCE: P1110  
CURRENT AFFILIATION NUMBER: 00000000000000000000  
CURRENT FILING DATE: 2001-11-19  
PRIORITY APPLICATION NUMBER: 00000000000000000000  
PRIORITY FILING DATE: 2001-11-16  
NUMBER OF SEQ ID NOS: 17  
SEQ ID NO: 12  
LENGTH: 29  
TYPE: DNA  
ORGANISM: Homo sapiens

US-89-997-964-12

67 1 AGGGAATTTCCTTGGGAAATTTCC 25  
2 ||||| ||||| ||||| |||||  
36 4 AGGGAATTTCCTTGGGAAATTTCC 2

RESUB: 6  
US 10-081-280 10

Sequence 10, Application US/10081200  
 Patent No. US20020165157A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi O.  
 TITLE OF INVENTION: APO-1 IN ANT APO-3 POLYMERIZED  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENT ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 460 Point San Bruno Blvd  
 City: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

TO PROPERTY: 12000  
SEQUENCE DESCRIPTION: SEC 10 NO. 10  
US-10-00 200 10

Dy 1 AGGGACATTCCGCTGGGSACTTCC 2  
4 TTTTCTTTTTTTTTC

Dd 4 AGGGACTTTCCGCTGGGSACTTCCC 2

RESULT 7  
US 09 987 979-12  
Applicant: Chundharpal, Anan  
General Information:  
Patent No. 09 987 979-12  
GENERAL INFORMATION:  
APPLICANT: Acharya, An J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chundharpal, Anan

1 PRIOR FILING DATE: 1976-06-06 08:33  
2 PRIOR FILING NUMBER: 0567039, 2  
3 PRIOR FILING DATE: 1976-06-06  
4 NUMBER OF SEQ IN NOS: 17  
5 SEQ ID NO: 12  
6 LENGTH: 23  
7 TREE: DNA  
8 ORGANISM: Homo sapiens  
9 US-07-887,879 12

Seq	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Seq	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Seq	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Seq	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Seq	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Seq	1	2	3	4	5	6																																																																																														

COMPUTER: IBM PC compatible  
SERIALS SYSTEM: DOS/MS-DOS  
SOFTWARE: WinData Genetech  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 05/09/99/274  
FILING DATE: 4 NO. 05/09/2001  
CLASSIFICATION: Unexamined  
PRIOR APPLICATION DATA:

RESULT 8  
 Sequence 10, Application ID: 050992234  
 Patient ID: 050992234-1881  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi  
 TITLE OF INVENTION: Apo 2, 3 AND Apo-3 POLYMERIZATION  
 NUMBER OF SEQUENCES: 1  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Genentech, Inc.  
 Attn: 460 Point San Bruno Blvd  
 City: South San Francisco  
 State: California  
 COUNTRY: USA  
 ZIP: 94086  
 COMPUTER READEABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: Microsoft Genentech  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/992,234  
 FILING DATE: 7 NO. US/2004/019678A1 2004  
 CLASSIFICATION: 2800000  
 PRIORITY APPLICATION DATA:

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1  APPLICATION NUMBER: 09/029,455
2  FILING DATE: 09/02/2000
3  ATTORNEY/AGENT INFORMATION:
4  NAME: Marschang, Diane L.
5  REGISTRATION NUMBER: 35,600
6  REFERENCE/POCKET NUMBER: P1001
7  TELECOMMUNICATION INFORMATION:
8  TELEPHONE: 415/932-9410
9  TELEFAX: 415/932-9441
10  INFORMATION FOR SEQ ID NO 1:
11  SEQUENCE CHARACTERISTICS:
12  LENGTH: 29 base pairs
13  TYPE: Nucleic Acid
14  STRANDEDNESS: Single
15  TOPOLOGY: Linear
16  SEQUENCE DESCRIPTION: SEQ ID NO 1:
US 09-993 234-10
Query Match 100.0% Score 25, DB 10, Length 29;
Best Local Similarity 100.0%, Freq. No. 0,0054;
Matches 25, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

27 1 AGGGACTTTCGGTGGGACTTTC 25
1b 4 AGGGACTTTCGGTGGGACTTTC 28

RESULT 9
US 10 080-495 6
Sequence 6, Application US/10090455
Patent No. US00020146199A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Gidycz, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Mark, Melanie R.
APPLICANT: Marsters, Scott A.
APPLICANT: Ellis, Robert M.
TITLE OF INVENTION: Methods for Treating and Diagnosing Autoimmune Disease
FILE REFERENCE: P1001-11-1A
CURRENT APPLICATION NUMBER: US/09/029,455
PRIOR FILING DATE: 2002-02-02
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: US 60/069,461
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: US 09/029,455
PRIOR FILING DATE: 1997-11-19
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 6
LENGTH: 29
TYPE: DNA
ORGANISM: Unknown
FEATURE:
NAME/KEY: misc feature
LOCATION: 1-29
OTHER INFORMATION: Description of Unknown Organism: Unknown
US 10 080-495-6
Query Match 100.0% Score 25, DB 10, Length 29;
Best Local Similarity 100.0%, Freq. No. 0,0054;
Matches 25, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

27 1 AGGGACTTTCGGTGGGACTTTC 25
1b 4 AGGGACTTTCGGTGGGACTTTC 28

RESULT 10
US 10 052-798 4
Sequence 4, Application US/10052798

```

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Patent No. US00000150985A1
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chantharapai, Anan
APPLICANT: Kim, Eyal J.
TITLE OF INVENTION: Apo 2 Receptor
NUMBER OF SEQUENCES: 14
REFERENCE/POCKET NUMBER: P1001
ADDRESS: Genentech, Inc.
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER FEASIBLE FORM:
MEDIUM TYPE: 3 1/2 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/052,798
FILING DATE: 02-NOV-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/POCKET NUMBER: P1001R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/932-9881
INFORMATION FOR SEQ ID NO 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO 4:
US 10 052-798-4
Query Match 100.0% Score 25, DB 12, Length 29;
Best Local Similarity 100.0%, Freq. No. 0,0054;
Matches 25, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

27 1 AGGGACTTTCGGTGGGACTTTC 25
1b 4 AGGGACTTTCGGTGGGACTTTC 28

RESULT 11
US 09-031-629A-5
Sequence 5, Application US/09031629A
Patent No. US000106689A1
GENERAL INFORMATION:
APPLICANT: Faustman
APPLICANT: Hayashi
TITLE OF INVENTION: Methods for Treating and Diagnosing Autoimmune Disease
FILE REFERENCE: MOH/Faustman 17633/1030
CURRENT APPLICATION NUMBER: US/09/031,629A
CURRENT FILING DATE: 1998-02-21
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Probe for
US 09-031-629A-5

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Query Match 100.0% Score 25 DP 10 Length 8933  
 Best Local Similarity 72.0% Pred No. 0.012  
 Matches 18 Conservative 7 Mismatches 11 Indels 0 Gaps 0

1 AGGACATTCGGCTGGGACATTCG 25  
 |||  
 6 AGGACATTCGGCTGGGACATTCG 25

RESULT 12  
 US-09-943-286-4  
 Sequence 16, Application US/09/943-41  
 Patent No. US2002015562A1  
 GENERAL INFORMATION:  
 APPLICANT: Lemon, Stanley  
 APPLICANT: YU, Minkyung  
 TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE  
 FILE REFERENCE: US/00/0101  
 CURRENT AFFILIATION NUMBER: US/99/443-41  
 CURRENT FILING DATE: 2000-12-23  
 PRIOR AFFILIATION NUMBER: US/99/11-393  
 PRIOR FILING DATE: 1999-12-23  
 NUMBER OF SEQ ID NOS: 34  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 18  
 LENGTH: 2239  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Nucleotide sequence of HIVSAP  
 HS-09-947-419-18

Query Match 100.0% Score 25 DP 10 Length 2239  
 Best Local Similarity 72.0% Pred No. 0.003  
 Matches 18 Conservative 7 Mismatches 11 Indels 0 Gaps 0

1 AGGACATTCGGCTGGGACATTCG 25  
 |||  
 6 AGGACATTCGGCTGGGACATTCG 256

RESULT 13  
 US-09-943-286-4  
 Sequence 9, Application US/09/943-41  
 Patent No. US2002015562A1  
 GENERAL INFORMATION:  
 APPLICANT: Nishimura, Kiyotada  
 TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD  
 FILE REFERENCE: GP104-02.UT  
 CURRENT AFFILIATION NUMBER: US/99/943-286  
 CURRENT FILING DATE: 2001-08-30  
 NUMBER OF SEQ ID NOS: 9  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 9  
 LENGTH: 8933  
 TYPE: RNA  
 ORGANISM: Human Immunodeficiency Virus  
 FEATURE:  
 NAME/KEY: source  
 LOCATION: (1).....(8933)  
 OTHER INFORMATION: Sequence of transcripts produced from the BH10  
 OTHER INFORMATION: plasmid  
 US-09-943-286-3

Query Match 100.0% Score 25 DP 10 Length 8933  
 Best Local Similarity 72.0% Pred No. 0.012  
 Matches 18 Conservative 7 Mismatches 11 Indels 0 Gaps 0

1 AGGACATTCGGCTGGGACATTCG 25  
 |||  
 6 AGGACATTCGGCTGGGACATTCG 8814

Query Match 100.0% Score 25 DP 10 Length 8933  
 Best Local Similarity 72.0% Pred No. 0.012  
 Matches 18 Conservative 7 Mismatches 11 Indels 0 Gaps 0

1 AGGACATTCGGCTGGGACATTCG 25  
 |||  
 6 AGGACATTCGGCTGGGACATTCG 8814

RESULT 14  
 US-09-943-286-4  
 Sequence 4, Application US/09/943-41  
 Patent No. US2002010669A1  
 GENERAL INFORMATION:  
 APPLICANT: Nishimura, Kiyotada  
 TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD  
 FILE REFERENCE: GP104-02.UT  
 CURRENT AFFILIATION NUMBER: US/99/943-286  
 CURRENT FILING DATE: 2001-08-30  
 NUMBER OF SEQ ID NOS: 9  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 4  
 LENGTH: 8933  
 TYPE: RNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Sequence of the 100-Amp pseudo amp  
 NAME/KEY: mutation  
 LOCATION: 413.....415  
 OTHER INFORMATION: Mutated position 413-415  
 OTHER INFORMATION: 4152-3, 4154  
 US-09-943-286-4

Query Match 100.0% Score 25 DP 10 Length 8933  
 Best Local Similarity 72.0% Pred No. 0.012  
 Matches 18 Conservative 7 Mismatches 11 Indels 0 Gaps 0

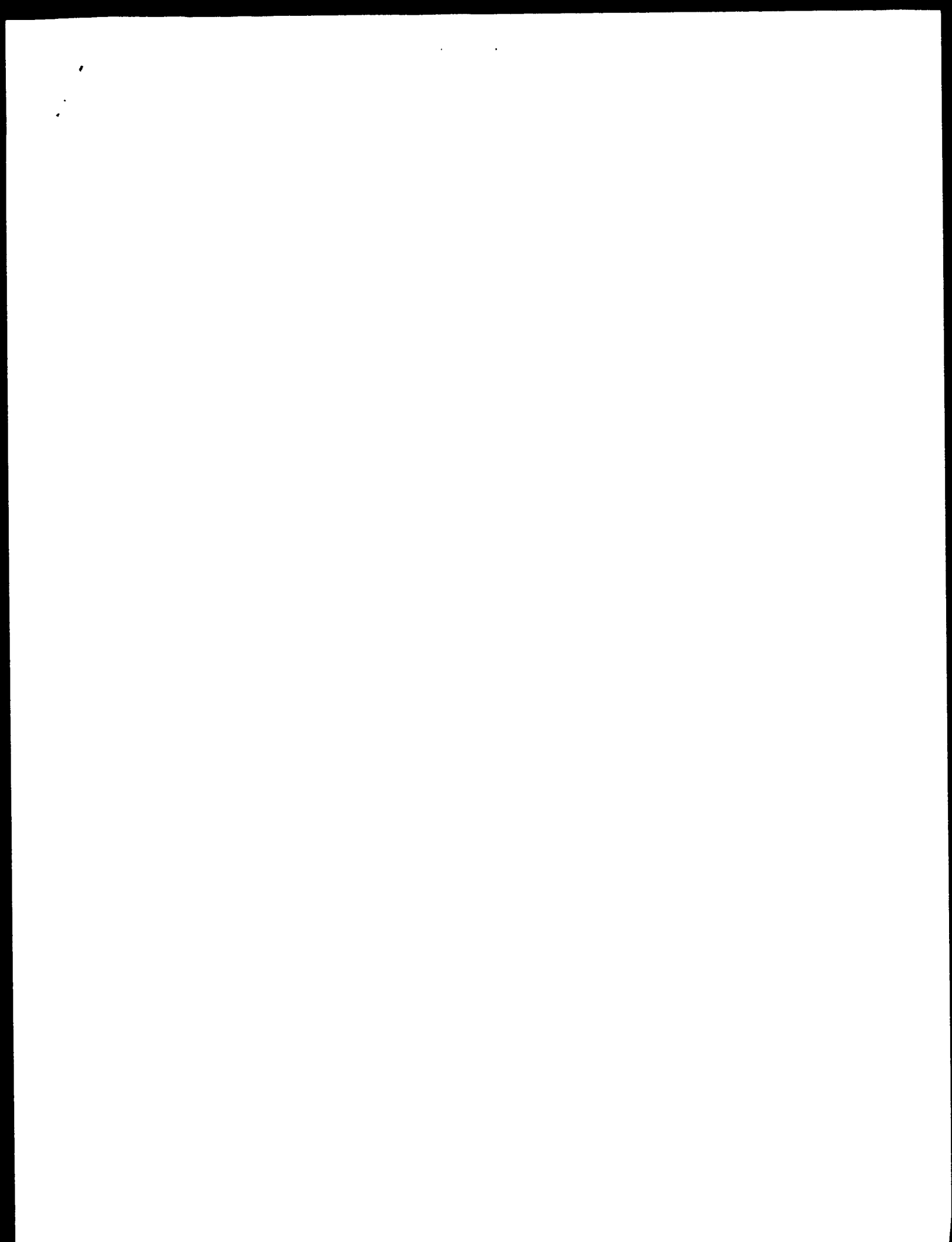
1 AGGACATTCGGCTGGGACATTCG 25  
 |||  
 6 AGGACATTCGGCTGGGACATTCG 8814

RESULT 15  
 US-09-943-286-9  
 Sequence 9, Application US/09/943-41  
 Patent No. US2002015562A1  
 GENERAL INFORMATION:  
 APPLICANT: Nishimura, Kiyotada  
 TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD  
 FILE REFERENCE: GP104-02.UT  
 CURRENT AFFILIATION NUMBER: US/99/943-286  
 CURRENT FILING DATE: 2001-08-30  
 NUMBER OF SEQ ID NOS: 9  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 9  
 LENGTH: 8933  
 TYPE: RNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Sequence of the 100-Amp pseudo amp  
 NAME/KEY: mutation  
 LOCATION: 4140.....(4150)  
 OTHER INFORMATION: Mutated position 414-415  
 OTHER INFORMATION: 4156-7, 4151  
 US-09-943-286-9

Query Match 100.0% Score 25 DP 10 Length 8933  
 Best Local Similarity 72.0% Pred No. 0.012  
 Matches 18 Conservative 7 Mismatches 11 Indels 0 Gaps 0

1 AGGACATTCGGCTGGGACATTCG 25  
 |||  
 6 AGGACATTCGGCTGGGACATTCG 8814

Search completed: December 1, 2002, 08:57:47  
 Job time: 56 secs







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Query Match          100.0%, Score 25, DB 1, Length 27;
Best Local Similarity 100.0%, Fred No. 0.0012,
Matches 25, Conservativeness 0, Mismatches 0, Indels 0,
Gaps 0;

CY 1 AGGAGCTTTCCTGGGACATTTC 25
DB 3 AGGAGCTTTCCTGGGACATTTC 27

RESULT 2
US 08 479 852-124
Sequence 124, Application US/08479852
Patent No. 5856088
GENERAL INFORMATION:
APPLICANT: Sherrill H. McDonough, Thomas B. Ryder,
APPLICANT: Teasing Yang
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
TITLE OF INVENTION: OLIGONUCLEOTIDES AND PROBES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
NUMBER OF SEQUENCES: 129
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB Storage
COMPUTER: IBM PS/2 Model 502 or 553X
OPERATING SYSTEM: IBM PC DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,852
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/040,745
FILING DATE: 28-MAR-1993
APPLICATION NUMBER: U.S. Serial No. 5856386 07/550,937
APPLICATION NUMBER: U.S. Serial No. 5856088 07/379,501
FILING DATE: 7/11/89
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 196/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 124.
LENGTH: 27
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE CHARACTERISTICS:
CY 1 AGGAGCTTTCCTGGGACATTTC 25
DB 3 AGGAGCTTTCCTGGGACATTTC 27

Query Match          100.0%, Score 15, DB 1, Length 27;
Best Local Similarity 100.0%, Fred No. 0.0012,
Matches 15, Conservativeness 0, Mismatches 0, Indels 0,
Gaps 0;

CY 1 AGGAGCTTTCCTGGGACATTTC 25
DB 3 AGGAGCTTTCCTGGGACATTTC 27

RESULT 3
US 08-462-646 44
Sequence 44, Application US/08462646
Patent No. 5856088
GENERAL INFORMATION:
APPLICANT: Sherrill H. McDonough, Thomas B. Ryder,
APPLICANT: Teasing Yang
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
TITLE OF INVENTION: OLIGONUCLEOTIDES AND PROBES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:

```

```

APPLICANT: Sherrill H. McDonough, Thomas B. Ryder,
APPLICANT: Teasing Yang
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
TITLE OF INVENTION: OLIGONUCLEOTIDES AND PROBES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB Storage
COMPUTER: IBM PS/2 Model 502 or 553X
OPERATING SYSTEM: IBM PC DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,646
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/040,745
FILING DATE: 28-MAR-1993
APPLICATION NUMBER: U.S. Serial No. 5856386 07/550,937
APPLICATION NUMBER: U.S. Serial No. 5856088 07/379,501
FILING DATE: 7/11/89
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 196/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 44.
LENGTH: 27
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE CHARACTERISTICS:
CY 1 AGGAGCTTTCCTGGGACATTTC 25
DB 3 AGGAGCTTTCCTGGGACATTTC 27

Query Match          100.0%, Score 25, DB 1, Length 27;
Best Local Similarity 100.0%, Fred No. 0.0012,
Matches 25, Conservativeness 0, Mismatches 0, Indels 0,
Gaps 0;

CY 1 AGGAGCTTTCCTGGGACATTTC 25
DB 3 AGGAGCTTTCCTGGGACATTTC 27

RESULT 4
US 08 462-646-124
Sequence 124, Application US/08462646
Patent No. 5856088
GENERAL INFORMATION:
APPLICANT: Sherrill H. McDonough, Thomas B. Ryder,
APPLICANT: Teasing Yang
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
TITLE OF INVENTION: OLIGONUCLEOTIDES AND PROBES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:

```

MEDIUM TYPE: 3 5" Diskette, 1.44 Mb, 512Kb  
COMPUTER: IBM PC/XT, M.B. 1.25, 1.25, 1.25  
OPERATING SYSTEM: IBM PC DOS (Version 3.10)  
SOFTWARE: WordPerfect (Version 5.0)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/462,646  
FILING DATE: 05-JUN-1993  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/09/460,745  
FILING DATE: 26-MAR-1993  
APPLICATION NUMBER: 09/460,997  
FILING DATE: 7/10/90  
APPLICATION NUMBER: 09/461,501  
FILING DATE: 7/11/89  
ATTORNEY/AGENT INFORMATION:  
NAME: Weidinger, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 156/189  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3810  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-462,646-124

Query Match: 100.0% Score: 25, Length: 27  
Best Local Similarity: 100.0% Pred. No. 0.0012  
Matches: 19, Conservative: 7, Mismatches: 0, Indels: 0, Gaps: 0

CY 1 AGGACCTTTCCTGGGACCTTTC 25  
|||||  
DB 3 AGGACCTTTCCTGGGACCTTTC 27

RESULT 5  
US-09-353-476-7  
Sequence 7, Application US/09/53476  
Patent No. 5971902  
GENERAL INFORMATION:  
APPLICANT: Weidinger, Susan  
ATTORNEY/AGENT INFORMATION:  
NAME: Weidinger, Arthur M.  
REGISTRATION NUMBER: 19,744  
REFERENCE/DOCKET NUMBER: GP-100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-353-476-7

Query Match: 100.0% Score: 25, Length: 27  
Best Local Similarity: 100.0% Pred. No. 0.0012  
Matches: 25, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

CY 1 AGGACCTTTCCTGGGACCTTTC 25  
|||||  
DB 2 AGGACCTTTCCTGGGACCTTTC 26

RESULT 6  
US-09-353-476-8  
Sequence 8, Application US/09/53476  
Patent No. 5971902  
GENERAL INFORMATION:  
APPLICANT: Weidinger, Susan  
ATTORNEY/AGENT INFORMATION:  
NAME: Weidinger, Arthur M.  
REGISTRATION NUMBER: 19,744  
REFERENCE/DOCKET NUMBER: GP-100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-353-476-8

Query Match: 100.0% Score: 25, Length: 27  
Best Local Similarity: 100.0% Pred. No. 0.0012  
Matches: 25, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

CY 1 AGGACCTTTCCTGGGACCTTTC 25  
|||||  
DB 2 AGGACCTTTCCTGGGACCTTTC 26

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-353-476-7

Query Match: 100.0% Score: 25, Length: 27  
Best Local Similarity: 100.0% Pred. No. 0.0012  
Matches: 25, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

CY 1 AGGACCTTTCCTGGGACCTTTC 25  
|||||  
DB 2 AGGACCTTTCCTGGGACCTTTC 26

RESULT 6  
US-09-353-476-8  
Sequence 8, Application US/09/53476  
Patent No. 5971902  
GENERAL INFORMATION:  
APPLICANT: Weidinger, Susan  
ATTORNEY/AGENT INFORMATION:  
NAME: Weidinger, Arthur M.  
REGISTRATION NUMBER: 19,744  
REFERENCE/DOCKET NUMBER: GP-100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-353-476-8

Query Match: 100.0% Score: 25, Length: 27  
Best Local Similarity: 100.0% Pred. No. 0.0012  
Matches: 25, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

CY 1 AGGACCTTTCCTGGGACCTTTC 25  
|||||  
DB 2 AGGACCTTTCCTGGGACCTTTC 26



```

1 NAME: Marschang, Diane L.
2 REGISTRATION NUMBER: 35,600
3 REPRESENTATION TYPE: Linear
4 REPRESENTATION INFORMATION:
5 TELECOMMUNICATION INFORMATION:
6 TELEPHONE: 650/225 5416
7 TELEFAX: 650/252 0981
8 INFORMATION REF ID: A001 4
9 SEQUENCE CHARACTERISTICS:
10 LENGTH: 29 base pairs
11 TYPE: Nucleic Acid
12 STRANDEDNESS: Single
13 TOPOLOGY: Linear
14
15 US-09-079-029-4

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Query Method	Time	Size	Index
Best Local	0.000	0.000	0.000
Method	0.000	0.000	0.000

```

Cy 1 AGGAACTTTTAA TGGAGATTTTTC 25
    |||||
Db 4 AGGAACTTTTAA TGGAGATTTTTC 28

```

RESULT 10  
US-08-928 069 14  
Sequence 14, Application US/08/0928000  
Date: 08/09/2008

1 GENERAL INFORMATION:  
2 APPLICANT: Ashkenazi, Avi J.  
3 TITLE OF INVENTION: APO3 POLYMERASE  
4 NUMBER OF CLAIMS: 15  
5 CORRESPONDENT ADDRESS:  
6 ADDRESS: Genentech, Inc.  
7 STREET: 1 DNA Way  
8 CITY: South San Francisco  
9 STATE: California  
10 COUNTRY: USA  
11 ZIP: 94060

COMPUTER: EASAPAR FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (genetec)  
CURRENT APPLICATION DATA:  
ACTIVATION NUMBER: 03-0000000-0004  
FILING DATE: 11-sep-1997  
CLASSIFICATION:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA  
APPLICATION NUMBER: 650,000,000  
FILING DATE: 09/23/1996  
ATTORNEY/AGENT INFORMATION  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,500  
REFERENCE/DOCKET NUMBER: P10221  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-9416  
TELEFAX: 650/957-9931  
INFORMATION FOR DOCKETING:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: Nucleic Acid  
STRANDNESS: Single  
TOPOLOGY: Linear  
18-08-924-963-14

Qy	Dh
1 AGGGAATTTCGGTGGGGAATTTC	4 AGGGAATTTCGGTGGGGAATTTC

RESULT 1:  
06-09-09 093A-10  
Sequence ID: APPL00000000708806833A  
Patent No. 6469144  
GENERAL INFORMATION:

GENERAL INFORMATION:  
 APPLICANT: ARBERGIAZI, AVI  
 TITLE OF INVENTION: APP. IN AND AP. POLYMERIZATION  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: CONTACT: 100

```

1      CURRENT APPLICATION DATA:
2      SOFTWARE: Mandarin Generation.
3      OPERATING SYSTEM: PC-DOS/MS-DOS
4      COMPUTER: IBM PC compatible
5      MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
6      COMMENTS RELEVANT FORM:

```

FILED AFFIDAVIT DATA: 03/02/2008  
AFFIDAVIT NUMBER: 03/02/2008  
FILING DATE: 1-APR-1996  
AFFIDAVIT NUMBER: 08/7118000  
FILING DATE: 03-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Markobaez, Diana

SEQUENCE	DESCRIPTION:	SEQ NO	NO
683A-10			

Seq	4	3	2	1	0	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
Seq	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99						

RESULT 12  
03-08-484-197A 25  
- 03-08-484-197A 25  
- 03-08-484-197A 25

GENERAL INFORMATION:  
APPLICANT: Juan, Shao-Chieh  
APPLICANT: Lichenstein, Henri S.  
APPLICANT: Wright, Samuel D.  
TITLE OF INVENTION: ANTI-INFLAMMATORY AND ANALGESIC  
NUMBER OF SEQUENCES: 38  
DEPOSITED IN THE ADDRESS:  
ADDRESSEE: AGENCO INC.

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.20  
CURRENT APPLICATION DATA:  
ATTORNEY/AGENT INFORMATION:  
FILING DATE: 07 JUN 1998  
CLASSIFICATION: 424  
NAME: Curry, Daniel R.  
REGISTRATION NUMBER: 32,727  
REFERENCE/DOCKET NUMBER: A-324A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 905/447-1000  
TELEFAX: 905/447-1000  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STANDARDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US 09 494 197A 25

Query Match: 100.0%; Score 25, DB 2, Length 33;  
Best Local Similarity: 100.0%; Pred. No. 0.0012;  
Matches: 25, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 AGGGACTTTTCGGTGGGGACTTTC 25  
|||  
DL 6 AGGGACTTTTCGGTGGGGACTTTC 40

RESULT 13  
US-09-484-197A-26/C  
Sequence 26, Application US/09484197A  
Patent No. 5824770  
GENERAL INFORMATION:  
APPLICANT: Juan, Shao-Chieh  
APPLICANT: Eichenstein, Henri S.  
APPLICANT: Wright, Samuel D.  
TITLE OF INVENTION: ANTI-INFLAMMATORY C14 POLYPEPTIDES  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: AMGEN INC  
STREET: 1840 DeHavilland Drive  
CITY: Thousand Oaks  
STATE: CA  
COUNTRY: US  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.20  
CURRENT APPLICATION DATA:  
ATTORNEY/AGENT INFORMATION:  
FILING DATE: 07 JUN 1998  
CLASSIFICATION: 424  
NAME: Curry, Daniel R.  
REGISTRATION NUMBER: 32,727  
REFERENCE/DOCKET NUMBER: A-324A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 905/447-1000  
TELEFAX: 905/447-1000  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STANDARDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

US-08-464-597A-26  
Query Match: 100.0%; Score 25, DB 2, Length 33;  
Best Local Similarity: 100.0%; Pred. No. 0.0012;  
Matches: 25, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 AGGGACTTTTCGGTGGGGACTTTC 25  
|||  
DL 32 AGGGACTTTTCGGTGGGGACTTTC 8

RESULT 14  
US-08-465-590-142  
Sequence 142, Application US/08465590  
Patent No. 5824770  
GENERAL INFORMATION:  
APPLICANT: Georgopoulos, Katia A.  
TITLE OF INVENTION: KINASES: A T CELL PATHWAY REGULATORY GENE  
NUMBER OF SEQUENCES: 164  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LARIVE & COCKFIELD  
STREET: 60 STATE STREET, Suite 510  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII (text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,590  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/238,212  
FILING DATE: 02-MAY-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/121,439  
FILING DATE: 14-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/946,233  
FILING DATE: 14-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Paul L.  
REGISTRATION NUMBER: 35,695  
REFERENCE/DOCKET NUMBER: MFG 8000LLV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 142:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 base pairs  
TYPE: nucleic acid  
STANDARDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US 08 465-590-142

Query Match: 100.0%; Score 25, DB 1, Length 36;  
Best Local Similarity: 100.0%; Pred. No. 0.0013;  
Matches: 35, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 AGGGACTTTTCGGTGGGGACTTTC 25  
|||  
DL 3 AGGGACTTTTCGGTGGGGACTTTC 27

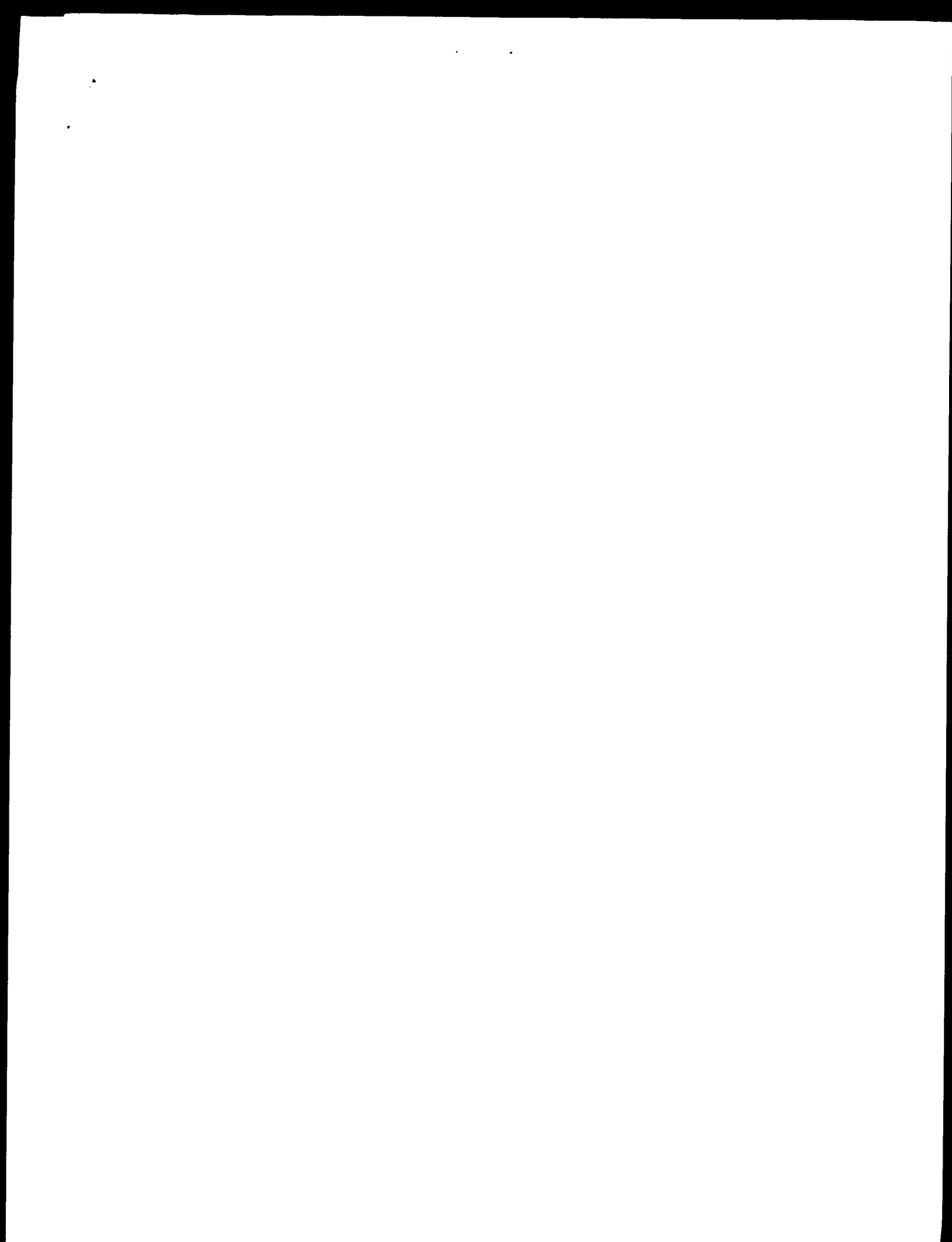
RESULT 15  
US-08-711-417C-142  
Sequence 142, Application US/08711417C  
Patent No. 6228611  
GENERAL INFORMATION:

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1  APPLICANT: Georgetown, Katie A.
2  TITLE OF INVENTION: METHOD A: RNA PATHWAY REGULATOR GENE
3  NUMBER OF SEQUENCES: 202
4  CORRESPONDENCE ADDRESS:
5  ADDRESS: Fish & Richardson P.C.
6  STREET: 225 Franklin Street
7  CITY: Boston
8  STATE: MA
9  COUNTRY: USA
10 ZIP: 02110-2804
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Diskette
14 COMPUTER: IBM compatible
15 OPERATING SYSTEM: Windows 95
16 SOFTWARE: FASTSEQ for Windows Version 2.0b
17
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/09/711,417C
20 FILING DATE: 05-SEP-1996
21
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: 08/219,212
24 FILING DATE: 02-MAY-1994
25 APPLICATION NUMBER: 08/121,438
26 FILING DATE: 14-SEP-1993
27 APPLICATION NUMBER: 07/346,233
28 FILING DATE: 14-SEP-1992
29
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Myers, Louis P.
32 REGISTRATION NUMBER: 35,965
33 REFERENCE: REF NUMBER: 1,111,111
34
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: 617/542-5070
37 TELEFAX: 617/542-8906
38 TELEX: 200154
39
40 INFORMATION FOR SEQ ID NO: 142:
41 SEQUENCE CHARACTERISTICS:
42 LENGTH: 36 base pairs
43 TYPE: nucleic acid
44 STRANDEDNESS: single
45 TOPOLOGY: linear
46 MOLECULE TYPE: cDNA
47
48 SEQUENCE DESCRIPTION: SEQ ID NO: 142:
49
50 US-09 711-417C-142
51
52 Query Match 100.0%; Score 25; DB 4; Length 36;
53 Best Local Similarity 100.0%; Pred No 0.0013;
54 Method 35; 2.000000000 3.000000000 0.000000000 0.000000000
55
56 CY 1 AGGAGCTTTCCTGAGGAGCTTTC 25
57 ||||||||||||||||||||
58 ||||||||||||||||||||
59
60 Db 3 AGGAGCTTTCCTGAGGAGCTTTC 27

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Search completed: December 1, 2002, 07:45:03  
Job time: 53 secs







XX XX  
 DR WPI, 2002-034509/04.  
 XX  
 XX Tolerogenic dendritic cell, useful for enhancing tolerogenicity in  
 PT mammalian host and treating asthma and septic shock, comprises  
 PT oligodeoxynucleotide having one or more nuclear factor kappaB  
 PT binding sites -  
 XX  
 XX Example 1; Page 17; 64pp; English.  
 XX  
 XX The invention relates to a tolerogenic dendritic cell (1) comprising an  
 CC oligodeoxynucleotide (ODN) having one or more nuclear factor (NF)-  
 CC kappaB binding sites. (1) is useful for enhancing tolerogenicity in a  
 CC mammalian host, (a transplant host or a host having Type 1 diabetes or an  
 CC inflammatory related disease such as arthritis). The method involves  
 CC preparing (1) and administering it to the host. The method further  
 CC involves administering PGE<sub>2</sub> and/or cyclosporin A to the host. (1) is  
 CC also useful for treating diabetes, enhanced foreign graft survival and for ameliorating  
 CC inflammation related diseases, such as autoimmune diseases e.g., lung  
 CC autoimmune arthritis, autoimmune diabetes, asthma, septic shock, lung  
 CC idiopathic glomerulonephritis, atherosclerosis and AIDS. The present  
 CC sequence represents an ODN comprising two NF-kappaB binding sites.  
 XX  
 XX Sequence 25 BP; 3 A; 7 G; 8 C; 7 T; 0 other;  
 XX  
 XX Query Match 100.0%; Score 25; DB 24; Length 25;  
 XX Best Local Similarity: 100.0%; Hit: 3; No. 0.047;  
 XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 AGGAGCTTCGCGCTGGGAGCTTCC 25  
 XX 1 AGGAGCTTCGCGCTGGGAGCTTCC 25  
 XX  
 XX RESULT 2  
 XX AB58185/c  
 XX ID AB58185 standard; DNA; 25 BP.  
 XX AC ABL58185;  
 XX  
 XX 30 JUL-2002 (first entry)  
 XX  
 XX NF-kappaB binding sites containing antisense ODN.  
 XX  
 XX Tolerogenicity; dendritic; nuclear factor, NF-kappaB; antidiabetic;  
 XX antiinflammatory; immunosuppressive; antiasthmatic; antibacterial;  
 XX nephropathy; antiatherosclerotic; anti-HIV; ds.  
 XX  
 XX Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 XX PH 1..10  
 XX FT /tag= a  
 XX FT /acc= "NF-kappaB binding site"  
 XX FT misc\_feature 15..24  
 XX FT /tag= b  
 XX FT /note= "NF-kappaB binding site"  
 XX  
 XX MOD0181713-A)  
 XX  
 XX 08-NOV-2001.  
 XX  
 XX 27 APR-2001; 2601WO-US1861.  
 XX  
 XX 28 APR-2001; 2000US-200479P.  
 XX  
 XX CFI: UNIV PITTSBURGH.  
 XX  
 XX Robbins PD, Lu L, Giamoukakis N;

XX XX  
 DR WPI, 2002-034509/04.  
 XX  
 XX Tolerogenic dendritic cell, useful for enhancing tolerogenicity in  
 PT mammalian host and treating asthma and septic shock, comprises  
 PT oligodeoxynucleotide having one or more nuclear factor kappaB  
 PT binding sites -  
 XX  
 XX Example 1; Page 17; 64pp; English.  
 XX  
 XX The invention relates to a tolerogenic dendritic cell (1) comprising an  
 CC oligodeoxynucleotide (ODN) having one or more nuclear factor (NF)-  
 CC kappaB binding sites. (1) is useful for enhancing tolerogenicity in a  
 CC mammalian host, (a transplant host or a host having Type 1 diabetes or an  
 CC inflammatory related disease such as arthritis). The method involves  
 CC preparing (1) and administering it to the host. The method further  
 CC involves administering PGE<sub>2</sub> and/or cyclosporin A to the host. (1) is  
 CC also useful for treating diabetes, enhanced foreign graft survival and for ameliorating  
 CC inflammation related diseases, such as autoimmune diseases e.g., lung  
 CC autoimmune arthritis, autoimmune diabetes, asthma, septic shock, lung  
 CC idiopathic glomerulonephritis, atherosclerosis and AIDS. The present  
 CC sequence represents an ODN comprising two NF-kappaB binding sites.  
 XX  
 XX Sequence 25 BP; 7 A; 8 C; 7 G; 3 T; 0 other;  
 XX  
 XX Query Match 100.0%; Score 25; DB 24; Length 25;  
 XX Best Local Similarity: 100.0%; Hit: 3; No. 0.047;  
 XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 AGGAGCTTCGCGCTGGGAGCTTCC 25  
 XX 25 AGGAGCTTCGCGCTGGGAGCTTCC 1  
 XX  
 XX RESULT 3  
 XX AA004699  
 XX ID AA004699 standard; DNA; 27 BP  
 XX  
 XX AA004699;  
 XX  
 XX 11-OCT-1990 (first entry)  
 XX  
 XX HIV enhancer negative element.  
 XX  
 XX Homo sapiens  
 XX  
 XX HIV; AIDS; beta-interferon; promoter; islet cells; gastrin; ds.  
 XX  
 XX W09005146-A  
 XX  
 XX 17-MAY-1990.  
 XX  
 XX 31-OCT-1989; 89WO-0904877.  
 XX  
 XX 31-OCT-1988; 88US-0265385.  
 XX  
 XX (GENO-) GEN HOSPTAL CORP.  
 XX  
 XX Brand SJ,  
 XX  
 XX WPI, 1990-178799/23.  
 XX  
 XX purified protein binding to nucleotide sequence -  
 XX with islet cell specific negative regulatory element of gastrin  
 XX gene.  
 XX  
 XX Disclosure; pp; English.  
 XX  
 XX Protein binding site is similar to human interferon gene element,  
 XX and may thus be used to regulate expression of interferon and other  
 XX genes containing such elements.  
 XX  
 XX Protein may be used to inhibit gastrin expression, and thus

CC unwanted development of gestin dependent islet cells in islet  
CC tumours and neonatal nesidioblastosis.  
CC see also AA044499.

XX Sequence 27 BP; 4 A; 0 C; 9 G; 7 T; 0 other;

Query March 100.0%; Score 25; DB 17; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.047;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACATTTCGGGACTTTC 25

DB 1 AGGACATTTCGGGACTTTC 25

RESULT 4

AAAT40192

ID AA40192 standard; DNA; 27 BP.

XX

AC AA40192;

XX

DT 25 APR-1997 (first entry)

XX

DE HIV target sequence #11.

XX

KW HIV, probe, primer, amplif., p-lymase chain reaction, microinjection,  
KW BCL-2; PCR; hepatitis B virus; HBV; CML; ss.

XX

OS Human immunodeficiency virus type 1.

XX

PN EF711175 A2.

XX

PC 11 SEP 1994.

XX

PF 10-JUL-1990; 90EP-0307503.

XX

PR 11-JUL-1990; 90US-0370501.

XX

PA (GENE) GEN-PROBE INC.

XX

PI M. Lomash S;

XX

CP WPI; 1996-403935/41.

XX

PT Detection of HIV nucleic acids in samples - using new specific  
PT oligonucleotide(s) for the amplification and detection of target  
PT sequences.

XX

PS (Gene) Page 17, 45pp, English.

XX

CC AAAT40192 (40192), and AAAT40193 (40193) represent HIV target sequences  
CC These sequences, and the sequences represented by AAAT40194 (40194) can be used as  
CC probes for HIV. The sequences for specific regions of the HIV genome  
CC These sequences can be used in kits of the invention, for detecting the  
CC presence of HIV nucleic acid sequences in a sample. The kits comprise  
CC two amplification primers such as AAAT40192 and AAAT40193, and a probe  
CC (such as AAAT40194) for detection of the amplified sequence. By using  
CC these sequences, the amplification of HIV nucleic acid sequences is  
CC improved. The kit can also be used for the detection of other  
CC microorganisms. By using different primer sequences, other sequences that  
CC can be detected using this method include those from PCR testing the  
CC sequences shown in AAAT40195 (40195), hepatitis B virus (using  
CC AAAT40196 (40196), and two flanking AAAT40197 (40197). The samples can be  
CC clinical, environmental or forensic samples, and the method produces  
CC large amounts of the target sequence for a variety of uses. The method  
CC can also be used to produce multiple copies of a target sequence for use  
CC in cloning, and sequencing, and to produce probes for the target  
CC sequence.

XX Sequence 27 BP; 4 A; 0 C; 9 G; 7 T; 0 other;

Query March 100.0%; Score 25; DB 17; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.047;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACATTTCGGGACTTTC 25

DB 1 AGGACATTTCGGGACTTTC 25

RESULT 5

AAAT30587

ID AAT30587 standard; DNA; 27 BP.

XX

AC AAT30587;

XX

DT 19-FEB-1997 (first entry)

XX

DE Target binding region #7.

XX

KW Target binding assembly; nucleic acid recognition unit; NF kappa B; SP1;  
KW TATA; human papillomavirus; HPV; HIV; human immunodeficiency virus;  
KW HIV LTR; Tat binding unit; probe; assembly sequence; assembly sequence;  
KW nuclear localisation signal sequence; human cell; HIV LTR; HIV; bacteria;  
KW virus; ss.

XX

OS Synthetic.

XX

PC WO9117056 A2.

XX

PD 13-JUN-1996

XX

PF 07-DEC-1995; 95WO-US15944.

XX

PR 09-DEC-1994; 94US-0353476.

XX

PA (GENE) GENE POOL INC.

XX

PI Weininger AM, Weininger S;

XX

DR WPI; 1996-287195/29.

XX

PT Probe nucleic acids; target binding assemblies, etc. for detection  
PT and localisation of specific nucleic acid sequences, esp. HIV and  
PT HPV

XX

PS Disclosure; Page 66; 172pp, English.

XX

CC AAAT30587 (30587) represent target binding regions. The probe of a probe of the  
CC invention. The probe of the invention contains a TBP, a boost of binding  
CC region (BBB), and an optional support or attachment (SAA). The target  
CC binding assembly (TBA) is recognised by the probe, contains at least one  
CC nucleic acid recognition unit (NAR), and optionally a linker sequence,  
CC AAAT30587 (30587), a nucleic acid assembly unit (NAR), and optionally a linker  
CC and an SAA. The assembly sequence and optionally a linker sequence  
CC AAAT30587 (30587) are selected from NF-kappa-B, SP1, TATA, human  
CC papillomavirus (HPV), HIV, HIV LTR, human immunodeficiency virus (HIV), HIV  
CC and Tat binding units. The linker sequence is an oligonucleotide, which  
CC does not interfere with NAR function, but provides stability and control  
CC over the spacing of the NAR from the rest of the TBA. The SAA is an  
CC attached support or linker, at least one of which is of localisation of the  
CC probe. The probe can be used in a method for detection of localisation of a  
CC specific target nucleic acid sequence (TNA). The method is highly  
CC sensitive, and has a high degree of specificity. The method can be used  
CC for detecting specific nucleic acid sequences, including those found in  
CC human cells, in HIV, HPV, and other nucleic acid containing systems,  
CC including bacteria and viruses.

XX Sequence 27 BP; 5 A; 7 C; 8 G; 7 T; 0 other;

Query March 100.0%; Score 25; DB 17; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.047;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGGACTTCCCTGGGACTTTC 25  
 2 AGGACTTCCCTGGGACTTTC 26

RESULT 6  
 AAT30588 standard: DNA; 2 BP.

AC AAT30588:

19 FEB-1997 (first entry)

Target binding region #8.

Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SPI;

TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;

HIV-1; Tat binding unit; Probe; assembly sequence; asymmetric sequence;

nuclear localisation signal sequence; human cell; HPV TBP; HIV; bacteria;

virus; ss

Synthetic.

NC061796.2.

13 JUN 1996.

07-DEC-1995: 95MO-US15944.

09-DEC-1994: 94US-0153476.

(GENE) GENE POOL INC.

Weininger AM, Weininger S;

WPI; 1996-287199/29.

Probe nucleic acids, target binding assemblies, etc - for detection

and localisation of specific nucleic acid sequences, esp. HIV and

HPV

Disclosures: Page 66; 17pp; English.

AAT30581-T30614 represent target binding regions (TBR) of a probe of the

invention. The probe of the invention contains a TBR, a locked binding

region (BBR), and an optional support or attachment (OSA). The target

binding assembly (TBA) recognised by the probe, contains at least one

nucleic acid recognition unit (NAR), and optionally a linker sequence, (see

an abstract of the invention, see AAT30614) and an asymmetric sequence (see

AAT30589-83067) a nuclear localisation signal sequence (see AAT30607).

AA074525: The assembly sequence and asymmetric sequences are

responsive for the folding and association of the NARs. The NARs (see

AA074525-83067) are selected from NF-kappa B, SPI, TATA, human

papillomavirus (HPV) E2, HIV LTR, human immunodeficiency virus (HIV) LTR

and Tat binding units. The linker sequence is an oligopeptide, which

does not interfere with NAR function, but provides stability and control

of the spacing of the NAR from the rest of the TBA. The OSA is an

attached support or nucleic acid, which is used for detecting or localising a

probe. The probe can be used in a method for detecting or localising a

specific target nucleic acid sequence (TNA). The method is highly

sensitive, and has a high degree of specificity. The method can be used

for detecting specific nucleic acid sequences, including those found in

human cells, in HIV, HPV, and other nucleic acid containing systems,

including bacteria and viruses.

Sequence 27 BP; 4 A; 7 C; 9 G; 7 T; 0 other;

Query: Match 100%; Score 25; DB 17; Length 27;

Best Local 25; Similarity 100%; Mismatches 0; Index 0; Gaps 0;

Matches 25; Conservative 0; Mismatches 0; Index 0; Gaps 0;

1 AGGACTTCCCTGGGACTTTC 25

2 AGGACTTCCCTGGGACTTTC 26

RESULT 7

AA074525 standard: DNA; 28 BP.

AA074525:

04-MAY-1995 (first entry)

Primer for the amplification of HIV-1 sequences.

Probe: primer; detection; amplification; identification; diagnosis;

HIV-1; human immunodeficiency virus; HIV-1; AIDS;

human T-cell leukaemia virus; acquired immune deficiency syndrome;

ss.

Synthetic.

Key

misc\_feature

Location/Qualifiers

/\*tag= 1

/notes= "It may be absent or is a 5' oligonucleotide

sequence which is specifically recognised by

an enzyme, e.g. the promoter sequence for T7,

is a site for polymerase, which enhances

initiation of elongation of RNA transcription

by an RNA polymerase. The sequence may be

e.g. 5'-AAATTATACACTGACTATACGACA-3'."

EPI17122-A.

28-SEP-1994.

26-MAR-1994: 94EP-0302196.

26-MAR-1993: 93US-0040745.

(GENE) GEN-PROBE INC.

Medonough SH, Ryder TB, Yang Y;

WPI; 1994-295780/37.

New oligonucleotides corresponding to HIV-1 sequences - used for

selective amplification and as hybridisation probes for detection

of HIV-1.

Claim 9; Page 4; 6pp; English.

Probes and primers specific for HIV-1 were identified by comparison

of published sequences of HIV-1, HIV-2, HIV-3 and HTLV-2 and were

then synthesised. The primers can be used for the selective

amplification of HIV-1 nucleic acid in a sample and may therefore be

useful in detection methods. See AA074525.

Sequence 28 BP; 4 A; 8 C; 8 G; 7 T; 1 other;

Query: Match 100%; Score 25; DB 15; Length 28;

Best Local 25; Similarity 100%; Mismatches 0; Index 0; Gaps 0;

Matches 25; Conservative 0; Mismatches 0; Index 0; Gaps 0;

1 AGGACTTCCCTGGGACTTTC 25

2 AGGACTTCCCTGGGACTTTC 26

AA074616

AA074616 standard: RNA; 29 BP.

AA074616:

XX  
 CI 25 MAY 1995 (first entry)  
 XX  
 DE Primer for the amplification of HIV-1 sequences.  
 XX  
 KW Probe, primer, detection, amplification, identification, diagnosis,  
 HIV-1, human immunodeficiency virus, HIV-1, AIDS,  
 KW Human T-cell leukemia virus; acquired immune deficiency syndrome,  
 XX  
 OS Synthetic.  
 XX  
 FH Key  
 FT misc feature  
 FT /tag= a  
 FT /note "May be absent or is a non-complementary  
 sequence which is specifically recognised by  
 an enzyme, e.g. the primer sequence for T7,  
 T3 or SP6 RNA polymerase, which enhances  
 initiation or elongation of RNA transcription  
 by an RNA polymerase. The sequence may be  
 e.g. 5'-AATTTAATAGGAGTCACTATAGGAGA-3'".  
 XX  
 PN EP617132 A.  
 XX  
 PD 28-SEP-1994.  
 XX  
 PF 28-MAR-1994; 14EP-0302195.  
 XX  
 PE 16 MAR 1994; 1208 204 045.  
 XX  
 PA GENPROBE GEN-PROBE INC.  
 XX  
 PI Mediatech SA, Ryder TR, Yang Y.  
 XX  
 DE WPI: 1994-035140/40.  
 XX  
 FT New oligonucleotides corresponding to HIV-1 sequences useful for  
 selective amplification and as hybridisation probes for detection  
 of HIV-1.  
 XX  
 PS Claim 3; Page 56; 5pp; English.  
 XX  
 CC Probes and primers specific for HIV-1 were identified by comparison  
 of published sequences of HIV-1, HIV-2, HIV-1 and HIV-2 and were  
 then synthesised. The primers can be used for the selective  
 amplification of HIV-1 sequences in a sample and may therefore be  
 useful in detection methods. See AG74500074500 and AG74500074500.  
 XX  
 SQ Sequence 28 BP; 4 A; 8 C; 9 G; 7 U; 1 other;  
 Query Match 100.0%, Score 25, DP 15, Length 28.  
 Best Local Similarity 72.0%, Pred. No. 0.048,  
 Matches 18; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 AGGACTTTCGCTGGGAGCTTTC 25  
 DB 4 AATTAATAGGAGTCACTATAGGAGA 28  
 RESULT 9  
 AG73477/c  
 XX  
 AC AA073477;  
 XX  
 DT 12-JUN-1995 (first entry)  
 XX  
 DE NF KB transcription factor binding motif  
 XX  
 KW NF KB transcription factor binding motif, antibody, detection,  
 XX  
 XX determination; ss.

OS Synthetic.  
 XX  
 PN EP620400-A  
 XX  
 PD 19-OCT-1994.  
 XX  
 PF 03 APR 1994; 04EP 0400027.  
 XX  
 PP 16 APR 1993; 93DE-4312399.  
 XX  
 PA (BEEF) BOEHRINGER MANNHEIM GMBH.  
 XX  
 PI Cafferis C, Hingorani V, Chakraborty H.  
 XX  
 DR WPI: 1994-318471/40.  
 XX  
 FT Determination of binding of transcription factor to nucleic acid by  
 incubating together, one component immobilised, and reaction with  
 labelled antibody, to detect activated cells for diagnosis of  
 cancer and autoimmune disease.  
 XX  
 PS Claim 12; Page 8; 9pp; German.  
 XX  
 CC The binding of the transcription factor (TF) to its binding motif is  
 determined by: (1) binding the TF or its binding motif to a solid  
 phase, (2) incubating TF and its binding motif, (3) adding a  
 labelled antibody specific for TF or its binding motif, if the  
 antibody is directed against the immobilised reactant then it will  
 compete with the other reactant for binding, (4) separating the  
 solid and liquid phases, and (5) determining the amount of label in  
 one of the phases as a measure of the binding between TF and its  
 binding motif.  
 XX  
 SQ Sequence 28 BP; 7 A; 9 C; 7 G; 5 T; 0 other;  
 Query Match 100.0%, Score 25, DP 15, Length 28.  
 Best Local Similarity 100.0%, Pred. No. 0.048,  
 Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 AGGACTTTCGCTGGGAGCTTTC 25  
 DB 27 AGGACTTTCGCTGGGAGCTTTC 3  
 RESULT 10  
 AA05947  
 XX  
 ID AA05947 standard; DNA, 28 BP.  
 XX  
 AC AA05947;  
 XX  
 DT 28-JUL-1999 (first entry)  
 XX  
 DE NF-kappaB specific oligonucleotide probe.  
 XX  
 KW DNA13355, tumor necrosis factor homologues; receptor, GTP;  
 XX immunogen, antibody, apoptosis, malignant cancer cells;  
 XX tumor necrosis factor (TNF)-alpha secretion, primary T cells;  
 XX proinflammatory response; probe; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9925834-A1.  
 XX  
 PD 27-MAY-1999.  
 XX  
 PE 18-NOV-1998; 96WO-US24621.  
 XX  
 PR 12 DEC 1997; 97US 0069661  
 XX 18-NOV-1997; 97US-0065635  
 XX  
 PA (GUTH) GENENTECH INC.  
 XX  
 PI Askenazi AJ, Baker KP, Godowski P, Gurney AL;



DB 4 AAGGACTTTCGTCGGGACTTCC 28

RESULT 13

AAV72528

ID AAV72528 standard; DNA; 29 BP.

AC AAV72528;

XX

DT 16-MAY-1993 (first entry)

DE

XX NF kappa B specific oligonucleotide probe #1.

XX Human Apo-2, monoclonal antibody, neutralizes tumour necrosis factor.

XX tumour necrosis factor, TNF, tumour necrosis factor receptor, TNFR.

XX TNF cytokine; probe; hybridization; 22.

XX

OS Synthetic.

OS Homo sapiens

XX

XX W020451793 A1.

XX

XX 19-NOV-1994.

XX

XX 14-MAY-1994; 9400-00000004.

XX

XX 09-FEB-1994; 9400-00000004.

XX

XX 15-MAY-1997; 9705-0857215.

XX

XX (GETH) GENENTECH INC.

XX

XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KS;

XX WPI; 1999 045228/04.

XX

XX Human Apo-2 polypeptide inducing apoptosis - useful to treat

XX conditions linked with impaired apoptosis and cancer, and produce

XX antibodies to increase or decrease apoptosis

XX

XX Example 6; Page 63; 131pp; English.

XX

XX The present invention describes human Apo-2. Apo-2 can be used

XX therapeutically to induce apoptosis in tumour cells, and is useful

XX to treat conditions associated with decreased apoptosis and cancer.

XX Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor

XX (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by

XX binding to TNFRs, and Apo-2 induces TNF receptor-dependent apoptosis. It

XX can be used to identify agents activating Apo-2, useful to treat

XX conditions linked with impaired apoptosis.

XX

XX Therapeutic uses of these containing immunoglobulin sequences can be

XX inhibit apoptosis or diagnostically useful for identifying agents

XX tag polypeptide with Apo-2 detection and purification using anti-Apo-2

XX antibodies. It can be used to produce antibodies which can be combined

XX with a pharmaceutically acceptable carrier in compositions

XX or used to produce immunocomplexes (especially immunotoxic

XX comprising first and second Apo-2 antibodies). Agents, especially

XX anti-chain antibodies, can be administered to induce apoptosis in

XX mammalian cancer cells, and anti-chain antibodies used to block

XX Apo-2 receptor. Apo-2 is a tumour necrosis factor (TNF) receptor

XX antibodies may also be used to identify agents that block Apo-2

XX extracellular domains and Apo-2 polypeptides. The present

XX example represents an NF-kappa2 specific oligonucleotide probe from an

XX example of the present invention.

XX

XX Sequence: 28 BP, 1 A, 2 G, 3 G, 4 G, 5 T, 6 T, 7 T, 8 T, 9 T, 10 T, 11 T, 12 T, 13 T, 14 T, 15 T, 16 T, 17 T, 18 T, 19 T, 20 T, 21 T, 22 T, 23 T, 24 T, 25 T, 26 T, 27 T, 28 T.

XX

XX

XX

XX

XX

RESULT 14

AAH24297

ID AAH24297 standard; DNA; 29 BP.

XX

AC AAH24297;

XX

DT 21-SEP-2001 (first entry)

DE

XX NF kappa B EMSA probe.

XX

XX NF kappa B inhibitor; nuclear factor kappa-B; GSK-3 inhibitor;

XX glycogen synthase kinase-3; hyperproliferative disorder; cancer;

XX inflammatory diseases; autoimmune diseases; asthma;

XX type 1 diabetes mellitus; myasthenia gravis; Sjogren's disease;

XX rheumatoid arthritis; allograft rejection; inflammatory bowel disease;

XX celiac disease; atrophic gastritis; multiple sclerosis; psoriasis;

XX systemic lupus erythematosus; SLE; glomerulonephritis; scleroderma;

XX vasculitis; inflammatory autoimmune myositis; autoimmune thyroiditis;

XX contact dermatitis; rhinitis; allergy; septic shock; systemic shock;

XX lung fibrosis; atherosclerosis; AIDS;

XX electrophoretic mobility shift assay; EMSA probe; ds.

XX

OS Synthetic.

XX

XX W0200147533 A2.

XX

XX 05-JUL-2001.

XX

XX 21-DEC-2000; 2000WO-CA01578.

XX

XX 23-DEC-1999; 9905 0172364.

XX

XX (ONTA) ONTARIO CANCER INST.

XX

XX Redflick K, Lu J, Woodgett J;

XX WPI; 2001-418157/44.

XX

XX Inhibiting nuclear factor-kappa-B activity in a cell for treating

XX asthma, lupus, scleroderma, tumor, psoriasis, inflammation, comprises

XX contacting the cell with an inhibitor of glycogen synthase kinase 3.

XX

XX Example 4; Page 21; 10pp; English.

XX

XX The invention relates to a method of inhibiting the activity of nuclear

XX factor kappa-B (NF kappa-B) in a cell via the use of an inhibitor of

XX glycogen synthase kinase 3 (GSK-3). In particular, NF kappa-B activity is

XX reduced by decreasing the activity of the beta subunit of GSK-3. GSK-3 is

XX the inhibitory activator of NF kappa-B. GSK-3 is associated with inflammatory

XX and hyperproliferative diseases. GSK-3 inhibitors and their use

XX in the method of the invention include lithium, valproic acid,

XX pyridine imide, dihydroquidine, and GSK-3 antibodies and GSK-3 antisense

XX oligonucleotides, as well as agents which indirectly inhibit GSK-3,

XX such as wortmannin and bongkic acid. The invention also encompasses

XX methods of screening for modulators of GSK-3 function, and a mammalian

XX transgenic animal which has a defect in GSK-3 function for use as a

XX model for GSK-3 function. The invention also includes enhanced methods

XX for the enhanced killing of cancer cells through the modulation

XX action of GSK-3 inhibitors, when GSK-3 inhibitors are administered in

XX conjunction with apoptosis-inducing ligands of TNF-related apoptosis

XX factor receptor. Each method is useful for treating

XX hyperproliferative disorders such as cancer and psoriasis. The use of

XX GSK-3 inhibitors to inhibit NF kappa-B function has applications in the

XX treatment of inflammatory and autoimmune disorders. The conditions that

XX may be treated using this method include asthma, type 1

XX diabetes mellitus, myasthenia gravis, Graves' disease, rheumatoid

XX arthritis, allograft rejection, inflammatory bowel disease, Crohn's

XX disease, ulcerative colitis, multiple sclerosis, psoriasis, systemic

XX lupus erythematosus (SLE), glomerulonephritis, scleroderma, various

XX forms of vasculitis, inflammatory myositis, myasthenia, autoimmune

XX thyroiditis, contact dermatitis, rhinitis, allergic rhinitis, septic shock,

CC systemic shock, lung fibrosis, atherosclerosis and AIDS. The present  
 CC sequence is an EMSA (electrophoretic mobility shift assay) probe  
 CC containing two tandem NF-kappa-B binding sites used to detect  
 CC NF-kappa-B activation in embryonic stem cells treated with  
 CC GSK-3b inhibitors.  
 CC  
 CC Sequence 29 bp; 4 A, 8 C, 9 G, 8 T; 0 other;  
 CC  
 CC Query Match 100.0%; Score 25; DB 22; Length 29;  
 CC Best Local Similarity 100.0%; Pval 3e-0648;  
 CC Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC 1 AGGAGCTTCCGCTGGGACTTTC 25  
 CC |||||  
 CC 4 AGGAGCTTCCGCTGGGACTTTC 29

## RESULT:5

AA84483

ID AA84483 standard; cDNA, 29 bp.

XX AA84483;

XX 29-JUN-2001 (first entry)

XX NF-kappa-B electrophoretic mobility shift assay (EMSA) probe

XX Human Apo-2 receptor; caspase-dependent apoptosis induction;

XX programmed cell death; pro-apoptotic; death domain;

XX antigenic antibody; nuclear factor kappa B;

XX NF-kappa B activation; cancer; tumor; lung cancer;

XX colon cancer; glioma; electrophoretic mobility shift assay;

XX EMSA probe; ds.

XX Homo sapiens.

XX WC200119861-A2.

XX 22-MAR-2001.

XX 11-SEP-2000; 2000WC025436.

XX 15-SEP-1999; 99US 0396710.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Chuntherapai A, Kim KJ;

XX WFL, 2001 26005/27.

XX Inducing apoptosis in mammalian cells for treating cancer, comprises

XX exposing mammalian cells or cancer cells expressing Apo-2 receptor, to

XX Apo-2 agonist antibody

XX Example 6; Page 53; 9pp; English.

XX

XX The invention relates to a method for inducing apoptosis in mammalian

XX cells which expresses the Apo-2 receptor protein (AA873442, AA873443).

XX The method involves exposing the cells to an Apo-2 agonistic antibody,

XX which induces Apo-2 receptor-mediated apoptosis. The Apo-2 receptor

XX (also referred to simply as Apo-2) is a member of the tumour

XX necrosis factor receptor (TNFR) family, and its natural ligand is the

XX Apo-2 ligand (Apo-2), also known as TRAIL. The Apo-2 receptor is able

XX to trigger caspase-dependent apoptosis, and is also able to activate

XX NF-kappa-B (nuclear factor kappa B). The Apo-2 receptor is an

XX domain in the cytoplasmic region (residues 324-332). It exhibits

XX significantly more sequence identity to the apoptosis-linked receptor

XX DR4, which also binds Apo-2L, than other apoptosis-associated proteins.

XX The Apo-2 receptor agonist monoclonal antibodies used in the method of

XX the invention are Tril 39.7, 39.14, 5, 3D5.1.10 and 3H.18.10. The

XX method of the invention is used to induce apoptosis in Apo-2-expressing

XX cells, particularly cancer cells. It may therefore be used for treating

XX

CC mammalian cancers, especially lung cancer, colon cancer and glioma.  
 CC The present sequence represents an NF-kappa-B electrophoretic mobility  
 CC shift assay (EMSA) probe used in an experiment which demonstrated that  
 CC the Apo-2 receptor was able to activate NF-kappa-B.  
 CC  
 CC Sequence 29 bp; 4 A, 8 C, 9 G, 8 T; 0 other;  
 CC  
 CC Query Match 100.0%; Score 25; DB 22; Length 29;  
 CC Best Local Similarity 100.0%; Pval 3e-0648;  
 CC Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC 1 AGGAGCTTCCGCTGGGACTTTC 25  
 CC |||||  
 CC 4 AGGAGCTTCCGCTGGGACTTTC 28

Search completed: December 1, 2002, 07:34:52  
 Job time : 270 secs





## UNIV FITTSBURGH OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION (US)

## FEATURES

Location/Qualifiers

1..25

/organism="synthetic construct"

/db\_xref="taxon:32630"

/note="Synthesized nucleotide sequence"

BASE COUNT 3 a 7 c 8 g 7 t

## ORIGIN

100.0% Score 25; DB 6; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

1 AGGACCTTCCGCTGCGACCTTCC 25

DB 3 AGGACCTTCCGCTGCGACCTTCC 27

## RESULT 3

AX299020

AX299020

25 bp DNA

Linear PAT 29-SEP-1999

DEFINITION Sequence 124 from patent US 5856088.

ACCESSION AR026280

VERSION AR026280.1 GI:5937110

## ORIGIN

100.0% Score 25; DB 6; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

1 AGGACCTTCCGCTGCGACCTTCC 25

DB 3 AGGACCTTCCGCTGCGACCTTCC 27

## RESULT 2

AX299020

AX299020

25 bp DNA

Linear PAT 29-SEP-1999

DEFINITION Sequence 124 from patent US 5856088.

ACCESSION AR026280

VERSION AR026280.1 GI:5937110

## ORIGIN

100.0% Score 25; DB 6; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

1 AGGACCTTCCGCTGCGACCTTCC 25

DB 3 AGGACCTTCCGCTGCGACCTTCC 27

## REFERENCE

Pattin, P.D., Le, L., and Glanville, R.

The use of recombinant plasmids for

cloning and methods for making the same

UNIV FITTSBURGH OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION (US)

Location/Qualifiers

1..25

/organism="synthetic construct"

/db\_xref="taxon:32630"

/note="Synthesized nucleotide sequence"

## ORIGIN

100.0% Score 25; DB 6; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

1 AGGACCTTCCGCTGCGACCTTCC 25

DB 3 AGGACCTTCCGCTGCGACCTTCC 27

## BASE COUNT

7 a 8 c 7 g 3 t

Query Match

100.0% Score 25; DB 6; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

100.0% Score 25; DB 6; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## ORIGIN

100.0% Score 25; DB 6; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

1 AGGACCTTCCGCTGCGACCTTCC 25

DB 3 AGGACCTTCCGCTGCGACCTTCC 27

## ORIGIN

100.0% Score 25; DB 6; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

1 AGGACCTTCCGCTGCGACCTTCC 25

DB 3 AGGACCTTCCGCTGCGACCTTCC 27

## ORIGIN

100.0% Score 25; DB 6; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

1 AGGACCTTCCGCTGCGACCTTCC 25

DB 3 AGGACCTTCCGCTGCGACCTTCC 27

## ORIGIN

100.0% Score 25; DB 6; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

1 AGGACCTTCCGCTGCGACCTTCC 25

DB 3 AGGACCTTCCGCTGCGACCTTCC 27

## ORIGIN

100.0% Score 25; DB 6; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

1 AGGACCTTCCGCTGCGACCTTCC 25

DB 3 AGGACCTTCCGCTGCGACCTTCC 27

## ORIGIN

100.0% Score 25; DB 6; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

1 AGGACCTTCCGCTGCGACCTTCC 25

DB 3 AGGACCTTCCGCTGCGACCTTCC 27

## ORIGIN

100.0% Score 25; DB 6; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

1 AGGACCTTCCGCTGCGACCTTCC 25

DB 3 AGGACCTTCCGCTGCGACCTTCC 27

## ORIGIN

100.0% Score 25; DB 6; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

1 AGGACCTTCCGCTGCGACCTTCC 25

DB 3 AGGACCTTCCGCTGCGACCTTCC 27

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KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (Bases 1 to 27)
AUTHORS      Weininger, S. and Weininger, A.M.
TITLE        Sequence Specific Detection of Mutations and Hybridizing a
             DNA-binding site. J. Mol. Biol. 271: 1-10 (1998)
JOURNAL      J. Mol. Biol. 271: 1-10 (1998)
FEATURES     Location/Qualifiers
             source 1..27
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BASE COUNT   4 a 7 c 9 g 7 t
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CY 1 AGGACTTTCCCTGGGACTTCC 25
DB 2 AGGACTTTCCCTGGGACTTCC 26

RESULT 7
LOCUS      E61341
DEFINITION Probe for detecting oligonucleotide.
ACCESSION E61341
VERSION    E61341.1 H113025905
KEYWORDS   synthetic construct.
SOURCE     Artificial construct.
ORGANISM   Artificial construct.
REFERENCE  1 (Bases 1 to 27)
AUTHORS    Daniel, J. and Timothy, J.F.
TITLE      Probe for detecting oligonucleotide
JOURNAL    GEN. PROTE. INC.
COMMENT    OS Artificial Sequence
           PN 27 10024078 A/17
           PD 21 FEB-1999
           PP 14 JAN-1998 JP 1998085607
           PP 11 JUL-1998 US 379501
           PI DANIEL, JAMES KASHIAN, TIMOTHY J. EUPHES
           PC 10/21/98, 01/20/99, 01/21/99
           CC 10/21/98, 01/20/99, 01/21/99
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           FT source 1..27
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           1..27
           /organism="Artificial Sequence"
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CY 1 AGGACTTTCCCTGGGACTTCC 25
DB 3 AGGACTTTCCCTGGGACTTCC 27

RESULT 9
LOCUS      192942
DEFINITION Sequence 41 from Patent US 5712385.
ACCESSION  192942
VERSION    192942.1 G1321233
KEYWORDS   nucleic acids
SOURCE     Patent: EP 0620439-A 2 19-OCT-1994;
           BOEHRINGER MANNHEIM GMBH (DE)
           Other publication DE 412499 941020.
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BASE COUNT 7 a 9 c 7 g 5 t  
ORIGIN

Query Match 100.0% Score 25, DP 6, Length 29,  
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Matches 25, Conservative 0, Mismatches 0, Indels 0, Gaps 0,  
Keywords

1 AAGACATTTTGGCTGGGACATTTTC 25  
DB 27 AAGACATTTTGGCTGGGACATTTTC 3

RESULT 11  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
SOURCE  
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Matches 25, Conservative 0, Mismatches 0, Indels 0, Gaps 0,  
Keywords

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DB 27 AAGACATTTTGGCTGGGACATTTTC 3

RESULT 12  
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VERSION  
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SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
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SOURCE  
BASE COUNT  
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Matches 25, Conservative 0, Mismatches 0, Indels 0, Gaps 0,  
Keywords

1 AAGACATTTTGGCTGGGACATTTTC 25  
DB 4 AAGACATTTTGGCTGGGACATTTTC 28

RESULT 13  
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VERSION  
KEYWORDS  
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JOURNAL  
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DB 26 AAGACATTTTGGCTGGGACATTTTC 2

RESULT 14  
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Query Match 100.0% Score 25, DP 6, Length 29,  
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Keywords

1 AAGACATTTTGGCTGGGACATTTTC 25  
DB 4 AAGACATTTTGGCTGGGACATTTTC 28

RESULT 13  
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Query Match 100.0% Score 25, DP 6, Length 29,  
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Matches 25, Conservative 0, Mismatches 0, Indels 0, Gaps 0,  
Keywords

1 AAGACATTTTGGCTGGGACATTTTC 25  
DB 26 AAGACATTTTGGCTGGGACATTTTC 2

RESULT 14  
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VERSION  
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SOURCE  
BASE COUNT  
ORIGIN

Query Match 100.0% Score 25, DP 6, Length 29,  
Best Local Similarity 100.0%, From Parent 0.13,  
Matches 25, Conservative 0, Mismatches 0, Indels 0, Gaps 0,  
Keywords

1 AAGACATTTTGGCTGGGACATTTTC 25  
DB 4 AAGACATTTTGGCTGGGACATTTTC 28

RESULT 15  
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ORIGIN

Query Match 100.0% Score 25, DP 6, Length 29,  
Best Local Similarity 100.0%, From Parent 0.13,  
Matches 25, Conservative 0, Mismatches 0, Indels 0, Gaps 0,  
Keywords

1 AAGACATTTTGGCTGGGACATTTTC 25  
DB 4 AAGACATTTTGGCTGGGACATTTTC 28

RESULT 16  
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AUTHORS  
TITLE  
JOURNAL  
FEATURES  
SOURCE  
BASE COUNT  
ORIGIN

Query Match 100.0% Score 25, DP 6, Length 29,  
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Keywords

1 AAGACATTTTGGCTGGGACATTTTC 25  
DB 4 AAGACATTTTGGCTGGGACATTTTC 28

RESULT 17  
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FEATURES  
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ORIGIN

Query Match 100.0% Score 25, DP 6, Length 29,  
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Matches 25, Conservative 0, Mismatches 0, Indels 0, Gaps 0,  
Keywords

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DB 4 AAGACATTTTGGCTGGGACATTTTC 28

RESULT 18  
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Keywords

1 AAGACATTTTGGCTGGGACATTTTC 25  
DB 4 AAGACATTTTGGCTGGGACATTTTC 28

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Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Juan S.-C., Lichenstein, H.S., and Wright, S.D.
TITLE Anti-inflammatory CD14 polypeptides
JOURNAL Parent: US 5869065, A 25 02 FEB 1999;
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06 6 AGGACCTTCCTCGCTGGGACCTTCC 30

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